

**REMARKS**

Claims 1-124 are pending and have been subject to restriction, addressed below. In addition, the specification (brief description of the drawings) has been amended as shown above to insert sequence identifiers.

**Restriction Requirement**

The Examiner, in the Restriction Requirement, required election of one of the following groups of claims:

Group I. Claims, 1-15, drawn to a method for isolating a collection of polynucleotides involving treating cellular chromatin with a probe;

Group II. Claims, 16-26, drawn to a method for isolating a collection of polynucleotides involving treating cellular chromatin with a methylase;

Group III. Claims, 27-30, drawn to a method for isolating a collection of polynucleotides involving treating cellular chromatin with a nuclease;

Group IV. Claims 31-37, drawn to a method for isolating a collection of polynucleotides involving treating cellular chromatin with a methylation-sensitive enzyme;

Group V. Claims 38-46, drawn to a method for isolating a collection of polynucleotides involving selectively cleaving AT-rich sequences of cellular DNA;

Group VI. Claims 47-53, drawn to a method for isolating a collection of polynucleotides involving fragmenting chromatin;

Group VII. Claims 54-58, drawn to a method of mapping accessible regions of cellular chromatin;

Group VIII. Claims 59-65, drawn to a method for generating a library of polynucleotides involving attaching an adapter;

Group IX. Claim 66, drawn to a library of polynucleotides;

Group X. Claims 67-71, drawn to a plurality of libraries of polynucleotides;

Group XI. Claim 72, drawn to a database of a collection of polynucleotide;

Group XII. Claims 73-77, drawn to a method of comparing a plurality of cell populations;

Group XIII. Claims 78-93, drawn to a method of analyzing polynucleotide sequences involving providing a database;

Group XIV. Claims 94-99, drawn to a method of analyzing polynucleotide sequences involving sequences corresponding to accessible regions of cellular chromatin; and

Group XV. Claims 100-124, drawn to a computer system for analyzing polynucleotide sequences.

Applicants hereby elect to prosecute the claims of Group IX, claim 66, with traverse.

Applicants submit that the above Restriction Requirement is unduly burdensome and in error. MPEP §803 states:

If the search and examination of an entire application can be made without serious burden, the examiner must examine it on the merits, even though it includes claims to independent and distinct inventions. (Emphasis added.)

The claims of Groups IX and X are all directed to libraries of polynucleotides. Indeed, claim 66 of Group IX, drawn to a library of polynucleotides, encompasses the claims of Group X, drawn to a plurality of these same libraries. Therefore, Applicants believe that the claims of Groups IX and X should be examined together as one group, as a single search is likely to find art related to both groups of claims, particularly in light of the fact that both groups share the same classification and subclassification (class 536, subclass 23.1). Moreover, the Office Action provided no reason supporting its assertion that Groups IX and X were independent and distinct.

Similarly, Applicants note that the claims of Groups I through VIII are all classified in class 435, subclass 6 and the claims in Groups XII to XV are all classified in class 702, subclass 19. Thus, Applicants submit that examination of the claims of Groups IX and X as one group, Groups I-VIII as another group and Groups XII to XV as a third group would not impose a serious burden on the Examiner, as a search of the art for references relevant to one claim in each group would necessarily reveal art relevant to the claims sharing the same classifications.

Indeed, Applicants believe that failure to examine the claims as proposed would pose a far greater burden on the Patent and Trademark Office, by requiring a duplication of effort and resources (*i.e.*, filing and examination of 14 additional applications), since a search directed to claims in Groups IX and X would turn up overlapping art if such art existed. Additionally, imposing a fifteen-way Restriction Requirement will cause a considerable expense to Applicants. Accordingly, Applicants respectfully traverse the above Restriction Requirement and request reconsideration thereof.

Applicants expressly reserve their right under 35 USC §121 to file one or more divisional applications directed to any nonelected subject matter during the pendency of this application.

Applicants response to Restriction Requirement, submitted October 14, 2003 was alleged to be non-responsive. In particular, it was alleged that the application failed to comply with the requirements of 37 C.F.R. § 1.821 *et seq.* due to lack of inclusion of sequence identifiers relating to "sequences" on page 88.

As shown above in the amendments to the specification the terms MKKKK, MKKK and MKK are not amino acid sequences. Rather, they are acronyms for enzymes that catalyze phosphorylation cascades involved in signal transduction pathways and, accordingly, do not require sequence identifiers. Furthermore, the specification has been amended as shown above to clarify these well known acronyms.


Thus, Applicants submit that the specification fully complies with the requirements of 37 C.F.R. § 1.821. Examination of the pending claims on the merits is requested.

Sequence Listing

Applicants believe that the paper copy of the Sequence Listing filed October 24, 2001 and the computer readable form from parent application 09/844,501 as entered into the instant application by the Office on June 7, 2002 include all the sequences disclosed in the application that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. §1.821(a)(1) and (a) (2). As required under 37 C.F.R. §1.821(f), Applicants assert that the content of the copy in computer readable form is identical to the content of the paper copy of the "Sequence Listing" and no new matter has been introduced.

Respectfully submitted,

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